2.   (Amended) The method of claim 36 further comprising synthesizing the highly ranked members of said hierarchy of compounds.

32.   (New Claim) A method of identifying a compound that modulates activity of a target RNA comprising:

identifying at least one molecular interaction site on said target RNA

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site;

comparing three dimensional representations of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site;

synthesizing said highly ranked members of said hierarchy of compounds;

contacting said target RNA with at least one of said highly ranked members to provide a complex between said target RNA and said member or members;

ionizing said complex;

fragmenting said ionized complex; and

determining whether highly ranked member or members bind to said molecular interaction site of said RNA.

33.   (New Claim) The method of claim 32 further comprising determining the strength of binding of at least one highly ranked member in comparison to the binding strength of other highly ranked members.

34.   (New Claim) A method of identifying a compound that modulates activity of a target RNA comprising:

identifying at least one molecular interaction site on said target RNA, wherein said target RNA comprises single-stranded RNA and is mRNA, pre-mRNA, tRNA, rRNA, or snRNA;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site;

comparing three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site.

synthesizing the highly ranked members of said hierarchy of compounds;

contacting said target RNA with at least one of said highly ranked members to provide a complex between said RNA and the member or members;

ionizing said complex;

fragmenting said ionized complex; and

determining whether highly ranked member or members binds to said molecular interaction site of said RNA.

35.   (New Claim) The method of claim 34 further comprising determining the strength of binding of at least one highly ranked member in comparison to the binding strength of other highly ranked members.

36.   (New Claim) A method of identifying a compound that modulates a function of a target RNA comprising:

identifying at least one molecular interaction site on said target RNA, wherein interaction of said compound with said molecular interaction site modulates said function of said target RNA;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing three dimensional representations of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form said interaction with said molecular interaction site.

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